Attachment chemistry

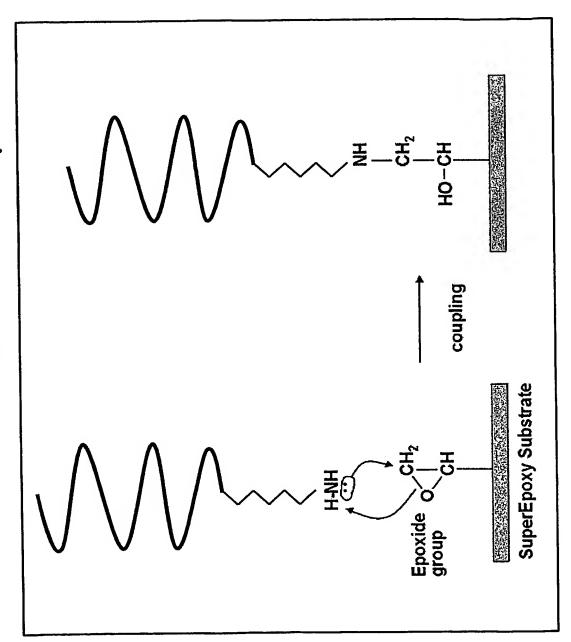


Figure 1

Microarray based genotyping Allele specific oligonucleotides (ASO)

Figure 2

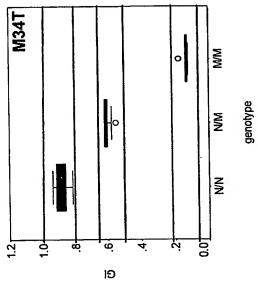
 $35\Delta G$ Step 1: Genotyping of connexin 26 35AG and M34T mutations (i) control LACINITACIN SACE PAGE LACINISACE ך ≥ Z r Z 0 $\langle \rangle$ T

Figure 3

Step 1: Genotyping of connexin 26 $35\Delta 6$ and M34T mutations (ii)

Genotype Index (GI) =
$$\frac{SV_N}{(SV_N + SV_M)}$$

35AG



9. 9.

Figure 4

MM

Σ

ž

genotype

Step 2: Genotyping of connexin 26 mutations

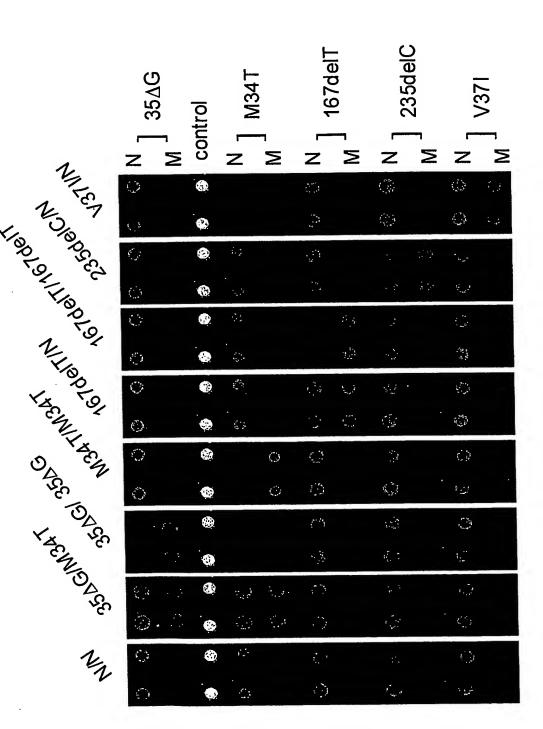
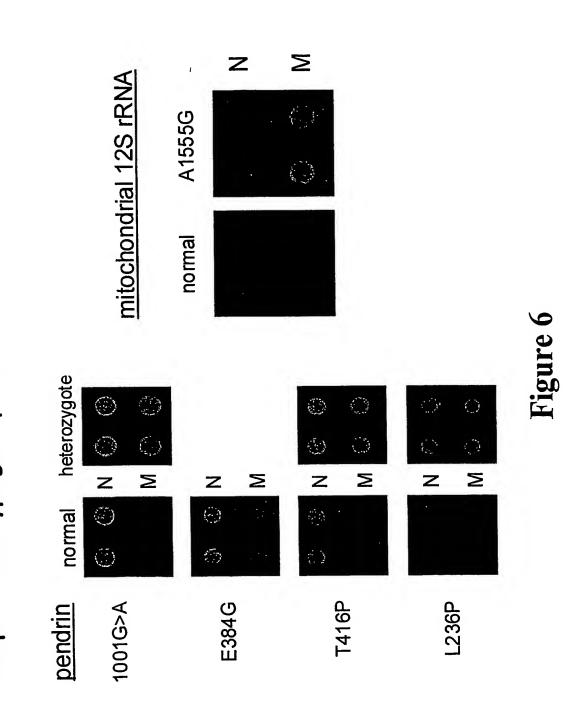
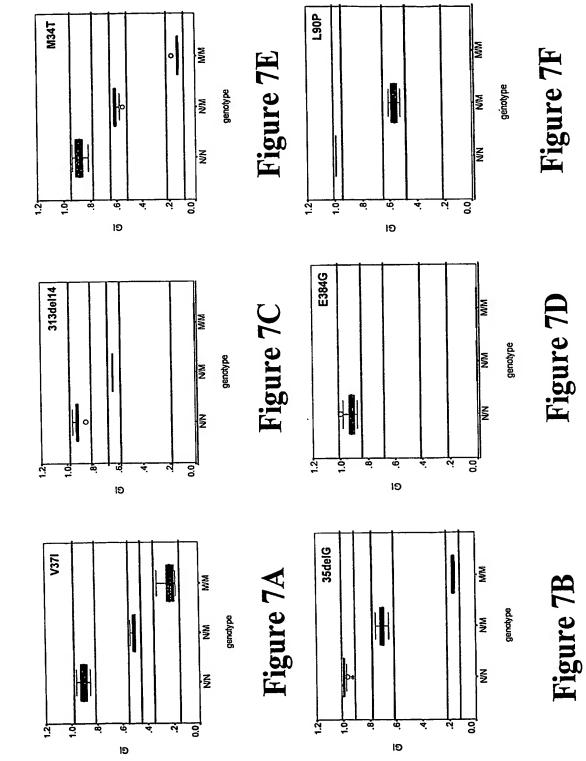


Figure 5

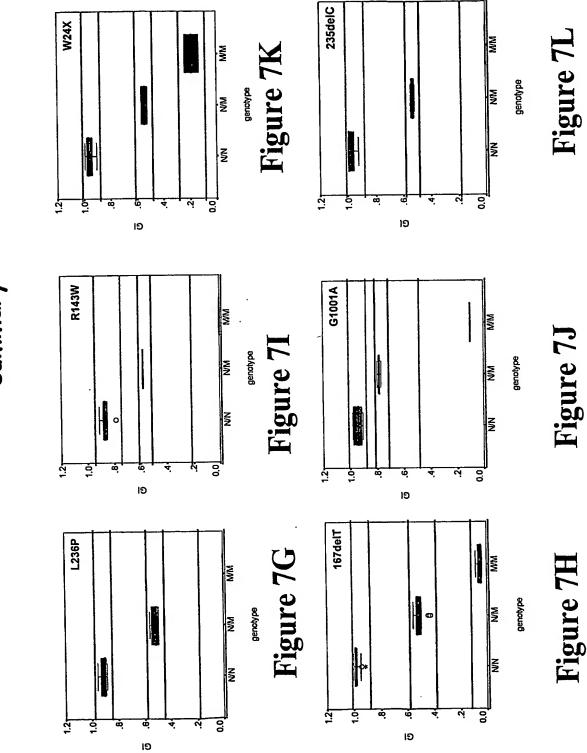
Step 2: Genotyping of pendrin and 125 rRNA mutations



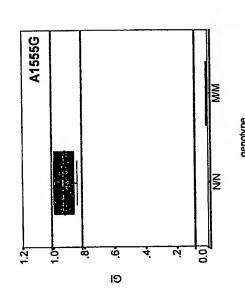




Genotyping summary



Genotyping summary



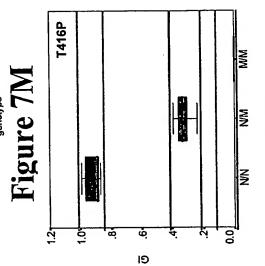
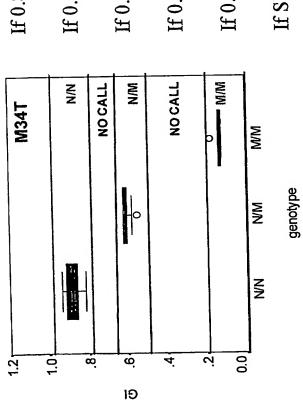


Figure 7N

Genotype calling algorithm



If 0.8 < GI < 1.0 then call = N/N

If 0.65 < GI < 0.8 then call = NO CALL

If 0.65 < GI < 0.5 then call = N/M

If 0.2<GI<0. 5 then call = NO CALL

If 0.0 < GI < 0.2 then call = M/M

If $SI_N + SI_M < 100$ then call = NO CALL

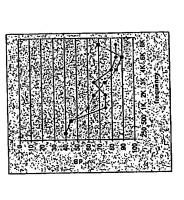
Figure 8

Interactions between deafness genes?

severe hearing loss

progressive

age of onset 10 years



| Call | Z | Z | <u>Z</u> | Ž | M/M | | ZZ |
|----------|------------------|----------|----------|----------|----------|----------|------------|
| 9 | 0.935414 | 0.906897 | 0.941176 | 0.969543 | 0.007764 | 100.00 | 0.995937 |
| Mutation | pendrin L236P | G1001A | E384G | T416P | 12S rRNA | Albabo | 2299delG |
| Call | | | 2/2 | N/N | ZZ | NN NN | Z Z Z Z |
| 5 | | .÷. | 0.32030 | | 0.999151 | | |

Figure 9